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Page 2

44. (New) A method for identifying a population of bi-ligands to dehydrogenases in a dehydrogenase enzyme family, comprising:

(a) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of a dehydrogenase in said dehydrogenase enzyme family, to form a module;

(b) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(c) screening said population of bi-ligands for binding to a dehydrogenase in said dehydrogenase enzyme family;

(d) identifying a bi-ligand that binds to and has specificity for said dehydrogenase; and

(e) repeating steps (c) and (d) to identify a bi-ligand that binds to and has specificity for a second dehydrogenase in said dehydrogenase enzyme family.

45. (New) The method of claim 44, wherein said expansion linker has approximate C2 symmetry.

46. (New) The method of claim 44, wherein said expansion linker has perfect C2 symmetry.

Inventor: Daniel S. Sem
Serial No.: 09/765,696
Filed: January 21, 2001
Page 3

47. (New) A method for identifying a population of bi-ligands to enzymes in an enzyme family, comprising:

(a) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of an enzyme in said enzyme family, to form a module, wherein said enzyme family binds the cofactor nicotinamide adenine dinucleotide or nicotinamide adenine dinucleotide phosphate;

(b) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(c) screening said population of bi-ligands for binding to an enzyme in said enzyme family;

(d) identifying a bi-ligand that binds to and has specificity for said enzyme; and

(e) repeating steps (c) and (d) to identify a bi-ligand that binds to and has specificity for a second enzyme in said enzyme family.

48. The method of claim 47, wherein said enzyme family binds nicotinamide adenine dinucleotide.

Inventor: Daniel S. Sem
Serial No.: 09/765,696
Filed: January 21, 2001
Page 4

49. The method of claim 47, wherein said enzyme family binds nicotinamide adenine dinucleotide phosphate.

50. (New) The method of claim 47, wherein said expansion linker has approximate C2 symmetry.

51. (New) The method of claim 47, wherein said expansion linker has perfect C2 symmetry.

52. (New) A method for identifying a population of bi-ligands to dehydrogenases in a dehydrogenase enzyme family, comprising:

(a) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of a dehydrogenase in said dehydrogenase enzyme family, to form a module, wherein said enzyme family binds the cofactor nicotinamide adenine dinucleotide or nicotinamide adenine dinucleotide phosphate;

(b) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(c) screening said population of bi-ligands for binding to a dehydrogenase in said dehydrogenase enzyme family;

Inventor: Daniel S. Sem
Serial No.: 09/765,696
Filed: January 21, 2001
Page 5

(d) identifying a bi-ligand that binds to and has specificity for said dehydrogenase; and

(e) repeating steps (c) and (d) to identify a bi-ligand that binds to and has specificity for a second dehydrogenase in said dehydrogenase enzyme family.

53. The method of claim 52, wherein said enzyme family binds nicotinamide adenine dinucleotide.

54. The method of claim 52, wherein said enzyme family binds nicotinamide adenine dinucleotide phosphate.

55. (New) The method of claim 52, wherein said expansion linker has approximate C2 symmetry.

56. (New) The method of claim 52, wherein said expansion linker has perfect C2 symmetry.

REMARKS

Claims 1-9, 11-14 and 37-43 are pending. Claims 9, 11-14, 37 and 41-43 are under examination. Claims 9, 11-14 and 37-43 have been canceled without prejudice to Applicant pursuing these claims in a related application. New claims 44-56 have been added. Support for the new claims can be found throughout the specification and the claims as filed. In particular, support for new claims 44, 47-49, and 52-54 can be found in original claims 9-12. Support for new claims 45, 46, 50, 51, 55